CLAIMS

What is claimed is:

1. A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous probes, wherein at least one of the two homologous probes is a non-linear probe, said method comprising:

introducing a mismatch with an intended target sequence in said non-linear probe; and

conducting a hybridization reaction using said at least two homologous probes.

2. A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous target sequences, said method comprising:

providing for an intended mismatch between at least one of the two homologous target sequences and at least one non-linear probe; and

conducting a hybridization reaction using said at least two homologous target sequences.

3. The method according to claim 1 or 2 in which the homologous probes are designed to detect point mutations in at least one target sequence.

4. The method according to claim 2, wherein at least two of said non-linear probes and/or two of said target sequences comprise an identical sequence except for a variation due to a point mutation or due to a mismatch in a nucleotide sequence.

5. The method according to any one of claims 1-4, wherein the mismatch in a nucleotide sequence comprises 1-3 nucleotides.

6. The method according to any one of claims 2-5, wherein the mismatch in a nucleotide sequence is located between 2 and 20 nucleotides upstream or downstream of a point mutation.

7. The method according to any one of claims 1-6 wherein the at least one non-linear probe has a length from about 15 to about 50 nucleotides.

8. The method according to any one of claims 1-7 wherein the at least one of the non-linear probes is provided with a detectable moiety.

9. The method according to any one of claims 1-8, further comprising amplifying a nucleic acid sequence.

10. A set of mixed homologous probes for detecting at least one allelic variant of a nucleic acid, wherein at least one of said set of mixed homologous probes is non-linear, said set of mixed homologous probes comprise at least one sequence completely complementary to and specific for one of the allelic variants of said nucleic acid, except for a specific mismatch located upstream, downstream or both upstream and downstream from the site of variation.

11. The set of mixed homologous probes of claim 10, wherein at least two of said set of mixed homologous probes comprise an identical sequence except for a variation due to a point mutation or a mismatch in a nucleic acid sequence.

12. The set of mixed homologous probes of claim 11, wherein said mismatch in a nucleic acid sequence comprises 1-3 nucleotides.

13. The set of mixed homologous probes of claim 11 or 12 wherein said mismatch in a nucleic acid sequence is located 2-20 nucleotides upstream or downstream of said point mutation.

14. The set of mixed homologous probes of any one of claims 10-13 wherein the set of mixed homologous probes have lengths between about 15 and about 50 nucleotides.

15. The set of mixed homologous probes of any one of claims 11-14 wherein said set of mixed homologous probes are in a single container.

16. A method of conducting a hybridization reaction comprising:

mixing a set of homologous probes for detecting at least one allelic variant of a nucleic acid, wherein at least one of said set of homologous probes is non-linear, said set of homologous probes comprise at least one sequence completely complementary to and specific for one of the allelic variants of said nucleic acid, except for a specific mismatch located upstream, downstream or both upstream and downstream from the site of variation;

detecting variants of the nucleic acids; and

using the set of homologous probes to conduct the hybridization reaction.

17. The method according to claim 16 wherein the nucleic acids are derived from a group of pathogens.

18. The method according to claim 17 wherein the nucleic acids represent a number of HIV-variants.

19. A kit for detecting at least one target sequence from a family of target sequences, said kit comprising at least one non-linear probe complementary to a target sequence specific for said family of target sequences and having a mismatch in a complementary sequence and further comprising suitable means for detection and/or amplification and/or isolation of nucleic acids.

20. The kit of claim 19, further comprising a set of mixed homologous probes for detecting at least one allelic variant of a nucleic acid, wherein at least one of said set of mixed homologous probes is non-linear, said set of mixed homologous probes comprising at least one sequence completely complementary to and specific for one of the allelic variants of said nucleic acid, except for a specific mismatch located upstream, downstream or both upstream and downstream from the site of variation.